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**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

# Office Action Summary

**Application No.**

10/532,198

**Applicant(s)**

SANCHEZ ET AL.

**Examiner**

SON T. HOANG

**Art Unit**

2165

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --  
**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 03 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 04 February 2009.  
2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.  
3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 85-112 is/are pending in the application.  
4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.  
5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.  
6) ☒ Claim(s) 85-112 is/are rejected.  
7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.  
8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.  
10) ☒ The drawing(s) filed on 21 April 2005 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).  
11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
a) ☐ All b) ☐ Some \* c) ☐ None of:  
1. ☐ Certified copies of the priority documents have been received.  
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.  
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- 1) ☒ Notice of References Cited (PTO-892)  
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)  
3) ☐ Information Disclosure Statement(s) (PTO-8508)  
Paper No(s)/Mail Date \_\_\_\_\_  
4) ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date \_\_\_\_\_  
5) ☐ Notice of Informal Patent Application  
6) ☐ Other: \_\_\_\_\_

## DETAILED ACTION

### *Response to Amendment*

1. This communication is in response to the amendment filed on February 4, 2009.

The abstract of the disclosure is amended.

**Claims 1-84** are canceled.

**Claims 85-112** are newly added.

**Claims 85-112** are pending.

### *Response to Arguments*

2. Objection to the abstract of the disclosure is withdrawn.
3. Objections to **claims 5, 8, 16, 18-19, 26, 64, and 81** are withdrawn.
4. The 35 U.S.C. 112, second paragraph, rejections of **claims 64, and 66-84** are withdrawn in view of Applicant's amendment.
5. Applicant's arguments with respect to the 35 U.S.C. 102(e) and 103(a) rejections to the claims have been considered but are moot in view of the new grounds of rejection presented hereon.

### *Claim Objections*

6. **Claim 110** is objected to because of the following informalities: not having a period (.) at the end of the claim's limitation. Appropriate correction is required.

### *Claim Rejections - 35 USC § 112*

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. **Claims 94-102** are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Regarding **claim 94**, it contains repeated limitations of "*periodically performing steps b-d*" in both steps *e* and *j*. Appropriate correction is required.

**Claims 95-102** are also rejected under 35 U.S.C. 112, second paragraph, for their dependencies on **claim 94**.

***Claim Rejections - 35 USC § 101***

9. **Claims 103-112** are rejected under 35 U.S.C. 101 because the claimed invention is directed to nonstatutory subject matters.

Regarding **claim 103**, "*a system for managing a biological database*" and multiple components, i.e. a target database node, a query node, a functional node, a network switch node, are being recited. However, these claimed components can easily be interpreted by an ordinary person skilled in the art as software per se and functional descriptive material consisting of data structures and computer programs, which impart functionality when employed as a computer component. As such, the claim is not limited to statutory subject matter and is therefore non-statutory.

The claimed system is directed to a software system itself, not a process occurring as a result of actually executing the software components, a machine programmed to operate in accordance with the software components, nor a manufacture structurally and functionally interconnected with the software components in a manner which enables the software components to carry out their functionalities.

The claimed system is also not a combination of chemical compounds to be a composition of matter. As such, it fails to fall within a statutory category. It is, at best, functional descriptive material *per se*.

**Claims 104-112** fail to resolve the deficiencies of **claim 103** since they only further limit the scope of **claim 103**. Hence, **claims 104-112** are also rejected under 35 U.S.C. 101.

The claims above lack the necessary physical articles or objects to constitute a machine or a manufacture within the meaning of 35 U.S.C. 101. They are clearly not a series of steps or acts to be a process nor are they a combination of chemical compounds to be a composition of matter. As such, they fail to fall within a statutory category. They are, at best, functional descriptive material *per se*.

Descriptive material can be characterized as either "functional descriptive material" or "nonfunctional descriptive material." Both types of "descriptive material" are nonstatutory when claimed as descriptive material *per se*, 33 F.3d at 1360, 31 USPQ2d at 1759. When functional descriptive material is recorded on some computer-readable medium, it becomes structurally and functionally interrelated to the medium and will be statutory in most cases since use of technology permits the function of the descriptive material to be realized. Compare *In re Lowry*, 32 F.3d 1579, 1583-84, 32 USPQ2d 1031, 1035 (Fed. Cir. 1994)

Merely claiming nonfunctional descriptive material, i.e., abstract ideas, stored on a computer-readable medium, in a computer, or on an electromagnetic carrier signal, does not make it statutory. See *Diehr*, 450 U.S. at 185-86, 209 USPQ at 8 (noting that

the claims for an algorithm in *Benson* were unpatentable as abstract ideas because “[t]he sole practical application of the algorithm was in connection with the programming of a general purpose computer.”)

***Claim Rejections - 35 USC § 103***

10. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

11. **Claims 85-87, 89-98, and 100-108, and 110-112** are rejected under 35 U.S.C. 103(a) as being unpatentable by Subramaniam et al. (*Pat. No. US 5,859,972, published on January 12, 1999; hereinafter Subramaniam*) in view of Gibson et al. (*Pub. No. US 2003/0055683, filed on September 19, 2002; hereinafter Gibson*).

Regarding **claim 85**, Subramaniam clearly shows and discloses a method for managing a biological database (*Abstract*), comprising:

a. receiving a set of biological sequences (*the user can build a complex query of up to seven terms. The user searches for all proteins relevant to the identifier “secretory trypsin inhibitor”, [Column 8, Lines 27-37]*);

b. querying a plurality of databases with the set of biological sequences (*Figure 5B shows the query builder screen, which permits the user to do a federated search for particular kinds of objects in two or more databases simultaneously, [Column 8, Lines 32-35]*);

c. receiving query results from the plurality of databases, wherein the query results comprise at least immunohistological data, *in situ* hybridization data, functional data, expression data, and structural data (*the objects searched for in the example of FIGS. 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database, [Column 8, Lines 48-51]*);

d. storing the query results in a biological database (*The server 18 may include a data store 101 for the use and storage of retrieved data by the user, [Column 4, Lines 40-41]*), wherein each sequence in the set of biological sequences is associated with a respective record comprising query results from each of the plurality of databases (*The search engine translates the idiom of particular databases into a federated query language. For example, the objects searched for in the example of Figures 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database. Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in Figures 5A-5C, [Column 8, Lines 47-57]*);

f. receiving, from a user, a request to view a record of one of the set of biological sequences; and g. displaying an executive summary of the record of one of the set of biological sequences (*The screen in Figure 5C shows the results of the search, with a scrollable window, "Collective Results", which shows all objects that were found from both databases during the search, [Column 8, Lines 37-40]*).

Subramaniam does not disclose the step of periodically performing steps b-d;

However, Gibson discloses the step of periodically updating searched results (*Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database, [0025]*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Gibson with the teachings of Subramaniam for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of Gibson).

Regarding **claim 86**, Subramaniam further discloses the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid sequences (*Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in FIGS. 5A-5C, [Column 8, Lines 51-57]*).

Regarding **claim 87**, Subramaniam further discloses receiving the set of biological sequences comprises receiving the set of biological sequences from a user



*(the user can build a complex query of up to seven terms. The user searches for all proteins relevant to the identifier "secretory trypsin inhibitor", [Column 8, Lines 27-37]).*

Regarding **claim 89**, Subramaniam further discloses the plurality of databases comprises two or more of National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases (*the databases 30 include molecular and structural biology databases, such as Gen Bank, PDB, and PIR. The services 32 may include BLAST*, [Column 5, Lines 15-19]).

Regarding **claim 90**, Subramaniam further discloses periodically performing steps b-d comprises performing steps b-d daily (*At step 95, the server update process 80 prepares data packets for the daily client update and compresses the data as required. At step 99, the server update process exits*, [0049]).

Regarding **claim 91**, Subramaniam further discloses performing one or more bioinformatics functions on the set of biological sequences or the query results (*In the screen of Figure 9A, the user has loaded into the workbench four objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for multiple sequence alignment, which returned the output shown on the screen in Figure 9B*, [Column 9, Lines 32-37]).

Regarding **claim 92**, Subramaniam further discloses the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis (*In the screen of Figure 9A, the user has loaded into the workbench four*

*objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for multiple sequence alignment, which returned the output shown on the screen in Figure 9B, [Column 9, Lines 32-37]].*

Regarding **claim 93**, Subramaniam further discloses displaying an executive summary of the record of one of the set of biological sequences comprises formatting the requested record for output to the user (*The informatics management system 10 receives the requested results from the remote repositories 19B and the repositories 19A on the server 18 back into the translator 16 which translates the retrieved results back into the user's format, e.g. HTML, [Column 4, Lines 21-26]].*

Regarding **claim 94**, Subramaniam clearly shows and discloses a method (*Abstract*) for managing a biological database, comprising:

f. receiving a set of biological sequences (*the user can build a complex query of up to seven terms. The user searches for all proteins relevant to the identifier "secretory trypsin inhibitor", [Column 8, Lines 27-37]]*);

g. querying the plurality of databases with the set of biological sequences (*Figure 5B shows the query builder screen, which permits the user to do a federated search for particular kinds of objects in two or more databases simultaneously, [Column 8, Lines 32-35]]*);

h. receiving query results from the plurality of databases, wherein the query results comprise at least immunohistological data, in situ hybridization data, functional

data, expression data, and structural data (*the objects searched for in the example of FIGS. 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database*, [Column 8, Lines 48-51]);

i. storing the query results in a biological database (*The server 18 may include a data store 101 for the use and storage of retrieved data by the user*, [Column 4, Lines 40-41]), wherein each sequence in the set of biological sequences is associated with a respective record comprising query results from each of the plurality of databases (*The search engine translates the idiom of particular databases into a federated query language. For example, the objects searched for in the example of Figures 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database. Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in Figures 5A-5C*, [Column 8, Lines 47-57]);

k. receiving, from a user, a request to view a record of one of the set of biological sequences; and l. displaying an executive summary of the record of one of the set of biological sequences (*The screen in Figure 5C shows the results of the search, with a scrollable window, "Collective Results", which shows all objects that were found from both databases during the search*, [Column 8, Lines 37-40]).

Subramaniam does not disclose the steps a-e and j.

However, Gibson discloses:

a. providing a plurality of databases (*The PRID system 10 includes client systems 16a, 16b, and 16c. Each client has applications and a local database 17a, 17b, and 17c, [0024];*

b. determining the version of each of the plurality of databases (*At step 82, the server update process 80 then accesses the appropriate databases to determine if there are updates to the predetermined list of databases. The predetermined list of databases includes, but is not limited to, the FDA, prescription drug databases, MSDS, or, O/S operating system databases or the like, [0047];*

c. determining if the version of each of the plurality of databases is a current version (*After accessing the predetermined databases, the server update process then determines if there is new data or updates to existing data at step 83, [0047];*

d. downloading the current version of any of the plurality of databases that is not a current version (*the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database, [0025];*

e. periodically performing b-d (*Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database, [0025]; and*

j. periodically performing steps b-d (*Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database, [0025]*).

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Gibson with the teachings of Subramaniam for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of Gibson).

Regarding **claim 95**, Subramaniam further discloses the plurality of databases comprises two or more of, National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases (*the databases 30 include molecular and structural biology databases, such as Gen Bank, PDB, and PIR. The services 32 may include BLAST, [Column 5, Lines 15-19]*).

Regarding **claim 96**, Gibson further discloses periodically performing steps b-d comprises performing steps b-d daily (*At step 95, the server update process 80 prepares data packets for the daily client update and compresses the data as required. At step 99, the server update process exits, [0049]*).

Regarding **claim 97**, Subramaniam further discloses the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid

sequences (*Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in FIGS. 5A-5C, [Column 8, Lines 51-57]*).

Regarding **claim 98**, Subramaniam further discloses receiving the set of biological sequences comprises receiving the set of biological sequences from a user (*the user can build a complex query of up to seven terms. The user searches for all proteins relevant to the identifier "secretory trypsin inhibitor", [Column 8, Lines 27-37]*).

Regarding **claim 100**, Subramaniam further discloses performing one or more bioinformatics functions on the set of biological sequences or the query results (*In the screen of Figure 9A, the user has loaded into the workbench four objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for multiple sequence alignment, which returned the output shown on the screen in Figure 9B, [Column 9, Lines 32-37]*).

Regarding **claim 101**, Subramaniam further discloses the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis (*In the screen of Figure 9A, the user has loaded into the workbench four objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for*

*multiple sequence alignment, which returned the output shown on the screen in Figure 9B, [Column 9, Lines 32-37]].*

Regarding **claim 102**, Subramaniam further discloses displaying an executive summary of the record of one of the set of biological sequences comprises formatting the requested record for output to the user (*The informatics management system 10 receives the requested results from the remote repositories 19B and the repositories 19A on the server 18 back into the translator 16 which translates the retrieved results back into the user's format, e.g. HTML, [Column 4, Lines 21-26]]*).

Regarding **claim 103**, Subramaniam further discloses a system for managing a biological database (*Figure 1*), comprising:

a target database node, configured to receive and store query results in the biological database, wherein the biological database comprises a set of biological sequences (*The server 18 may include a data store 101 for the use and storage of retrieved data by the user, [Column 4, Lines 40-41]*) and wherein the query results comprise at least immunohistological data, in situ hybridization data, functional data, expression data, and structural data (*The search engine translates the idiom of particular databases into a federated query language. For example, the objects searched for in the example of Figures 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database. Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the*

*common identifier "proteins" for purposes of the federated search shown in Figures 5A-5C, [Column 8, Lines 47-57]).*

Gibson discloses:

a query node, configured to periodically download and store a plurality of databases from an external network (*Figure 1 shows the PRID system 10 includes client systems 16a, 16b, and 16c. Each client has applications and a local mirror database 17a, 17b, and 17c, [0024]. Periodically, an update file is created for each client with all relevant changes since the last modification of the client database. When the clients systems 16(a-c) connect to the server 11, the modification files associated with the client are transmitted to the client to be used for updating each client's individual database, [0025];*

a functional node, configured to periodically query the plurality of databases on the query database node with the set of biological sequences from the target database node and send query results to the target database node (*the client prescription drug information dissemination system 140 requests periodic updates on a predetermined schedule from a server 11. These updates are then applied to the mirror prescription drug information database 17, so that the clients mirror prescription drug information database 17 is a mirror of the server prescription drug information database 12, [0042];* and

a network switch node configured to direct the receipt and storage of query results in the biological database, the periodic download and storage of the plurality of databases, and the periodic query of the plurality of databases



on the query database node (*A computer server 11 contains applications and a server DB 12 that are accessed by client systems 16(a-c) via intermittent connections, respectively, over network 14. The server 11 runs administrative software for a computer network and provides access to part or all of the network and its devices. The client systems 16(a-c) access the data on computer server 11 and may provide over a network 14, such as but not limited to: the Internet, a local area network (LAN), a wide area network (WAN), or public switched telephone network (PSTN) via a telephone line using a modem or other like networks, [0024].*

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Gibson with the teachings of Subramaniam for the purpose of creating update drug data for addition to the original drug information, and a transmit mechanism that transmits the update drug data to the remote device upon receiving a request from a remote device for the update drug data ([Abstract] of Gibson).

Regarding **claim 104**, Subramaniam further discloses the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid sequences (*Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in FIGS. 5A-5C, [Column 8, Lines 51-57]*).

Regarding **claim 105**, Subramaniam further discloses the functional node is further configured to perform one or more bioinformatics functions on the set of biological sequences or the query results and update the target database node (*In the screen of Figure 9A, the user has loaded into the workbench four objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for multiple sequence alignment, which returned the output shown on the screen in Figure 9B, [Column 9, Lines 32-37]).*

Regarding **claim 106**, Subramaniam further discloses the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis (*In the screen of Figure 9A, the user has loaded into the workbench four objects (in this case database entries for particular proteins) from the list that was collected in Figure 5C. Then the user entered these objects as data into a program for multiple sequence alignment, which returned the output shown on the screen in Figure 9B, [Column 9, Lines 32-37]).*

Regarding **claim 107**, Subramaniam further discloses the plurality of databases comprises two or more of, National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases (*the databases 30 include molecular and structural biology databases, such as Gen Bank, PDB, and PIR. The services 32 may include BLAST, [Column 5, Lines 15-19]).*

Regarding **claim 108**, Subramaniam further discloses the query node is further configured to periodically download and store a plurality of databases from an external network daily (*At step 95, the server update process 80 prepares data packets for the daily client update and compresses the data as required. At step 99, the server update process exits, [0049]*).

Regarding **claim 110**, Subramaniam further discloses each of sequences in the set of biological sequences is associated with a record comprising query results from each of the plurality of databases (*The search engine translates the idiom of particular databases into a federated query language. For example, the objects searched for in the example of Figures 5A-5C are designated "sequences" in the idiom of the PIR database and "compounds" in the idiom of the PDB database. Because the sequences listed in the PIR database are the amino acid sequences that define proteins, and because the compounds in the PDB database are proteins, the search engine translates the fields "compounds" (PDB) and "sequences" (PIR) into the common identifier "proteins" for purposes of the federated search shown in Figures 5A-5C, [Column 8, Lines 47-57]*).

Regarding **claim 111**, Subramaniam further discloses the target database node is further configured to:

receive, from a user, a request to view a record of one of the set of biological sequences; and display an executive summary of the record of one of the set of biological sequences (*The screen in Figure 5C shows the results of the search, with a*

*scrollable window, "Collective Results", which shows all objects that were found from both databases during the search, [Column 8, Lines 37-40]].*

Regarding **claim 112**, Subramaniam further discloses the target database node is further configured to format the requested record for output to the user (*The informatics management system 10 receives the requested results from the remote repositories 19B and the repositories 19A on the server 18 back into the translator 16 which translates the retrieved results back into the user's format, e.g. HTML, [Column 4, Lines 21-26]]*).

12. **Claims 88, 99, and 109** are rejected under 35 U.S.C. 103(a) as being unpatentable by Subramaniam et al. (*Pat. No. US 5,859,972, published on January 12, 1999; hereinafter Subramaniam*) in view of Gibson et al. (*Pub. No. US 2003/0055683, filed on September 19, 2002; hereinafter Gibson*), and further in view of Algate et al. (*Pub. No. US 2003/0118599, filed on May 10, 2002; hereinafter Algate*).

Regarding **claims 88, 99, and 109**, Subramaniam disclose the query results comprise pharmacology data (*Figure 13*).

Subramaniam, as modified by Gibson, does not disclose the query results further comprise complementary deoxyribonucleic acid (eDNA) data, expressed sequence tags.

However, Algate discloses the query results further comprise complementary deoxyribonucleic acid (eDNA) data (*Initial characterization of the cDNA expression library was performed by randomly sequencing 24 primary transformants and subjecting the resulting sequences to BLAST searches against available databases. The*

*determined cDNA sequences are provided in SEQ ID NO: 443-480, with the results of the BLAST searches being provided in Table 4, [0998]), expressed sequence tags (Comparison of the isolated sequences with those in the public database revealed no significant homologies to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID NO: 149, 152, 156, 157 and 158 were found to show some homology to previously isolated expressed sequence tags (ESTs), [0973]).*

It would have been obvious to an ordinary person skilled in the art at the time of the invention was made to incorporate the teachings of Algate with the teachings of Subramaniam, as modified by Gibson, for the purpose of utilizing polypeptides and polynucleotides to produce pharmaceutical compositions, e.g., vaccines, and other compositions for the diagnosis and treatment of lung cancer ([0002] of Algate).

### **Conclusion**

13. **THIS ACTION IS MA DE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

***Contact Information***

14. Any inquiry concerning this communication or earlier communications from the Examiner should be directed to Son T. Hoang whose telephone number is (571) 270-1752. The Examiner can normally be reached on Monday – Friday (7:00 AM – 4:00 PM).

If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Christian Chace can be reached on (571) 272-4190. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/S. T. H./  
Examiner, Art Unit 2165  
April 9, 2009

/Christian P. Chace/  
Supervisory Patent Examiner, Art Unit 2165